

2362-Pos**X-Ray Fiber Diffraction Reveals Major Structural Differences Between Brain-Derived Prions and Recombinant Prion Protein Amyloid**

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X-ray fiber diffraction was used to study the structure of brain-derived prions and recombinant prion protein amyloid. Partially oriented, dried fibers were prepared from brain-derived PrP 27-30 and recombinant PrP amyloid. Fiber diffraction patterns were analyzed and used to interrogate models for the structure of the infectious prion.

Fiber diffraction patterns of recombinant PrP amyloid displayed characteristic, meridional reflections at ~ 4.8 Å and equatorial reflections at ~ 10 Å. These patterns were similar to those of other amyloids and are consistent with a basic cross- β architecture. In contrast, diffraction patterns from brain-derived PrP 27-30 displayed meridional reflections at ~ 9.6 , ~ 6.4 , and ~ 4.8 Å, which correspond to the 2nd, 3rd, and 4th order of a ~ 19.2 -Å repeating unit, suggesting that PrP 27-30 contains four β -strands in a cross- β architecture. Furthermore, PrP 27-30 lacked the typical, equatorial reflection at ~ 10 Å, but instead produced equatorial reflections characterizing the diameter of the amyloid fiber and of individual protofilaments. Therefore, PrP 27-30 seems to have a structure consistent with a β -helix or β -solenoid, not unlike the model that was proposed earlier (Govaerts et al., 2004). This interpretation was also supported by extensive modeling, simulation of diffraction, electron microscopy, and FTIR.

In a previous study, recombinant PrP amyloid induced a transmissible prion disease in transgenic mice overexpressing PrP, and was thus termed a "synthetic prion" (Legname et al., 2004). Serially transmitted, synthetic prions were purified from mouse brains and analyzed by fiber diffraction. These brain-derived, synthetic prions showed the same structural characteristics as natural prion isolates and not those of its recombinant protein precursor. The relationship between structural differences and prion infectivity can be explained by several hypotheses. It remains to be determined which one, if any, is correct.

2363-Pos**Mutant Huntingtin Fragments Form Oligomers in a Polyglutamine Length-Dependent Manner**

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A feature of many neurodegenerative diseases is the rearrangement of a specific protein to a non-native conformation, promoting aggregation, amyloid fibril formation, and deposition within tissues or cellular compartments. Such diseases include Alzheimer's disease (AD), Parkinson's disease (PD), and Huntington's disease (HD). Huntington's disease (HD) is caused by an expansion above 35-40 polyglutamine (polyQ) repeats in the huntingtin (htt) protein and results in accumulation of inclusion bodies that contain fibrillar deposits of mutant htt fragments. Intriguingly, polyQ length is directly proportional to the propensity for htt to form fibrils and to the severity of HD, and is inversely correlated to the age of onset. Although the structural basis for htt toxicity is unclear, the formation, abundance and/or persistence of toxic conformers that mediate neuronal dysfunction and degeneration in HD must also be polyQ length-dependent. Here we used atomic force microscopy (AFM) to show that mutant htt fragments and synthetic polyQ peptides form oligomers in a polyQ length-dependent manner. Time-lapse AFM shows oligomers form before fibrils, are transient in nature, and are occasionally direct precursors to fibrils. However, the vast majority of fibrils appear to form by monomer addition that coincides with the disappearance of oligomers. Thus, oligomers must undergo a major structural transition that precedes fibril formation. These results demonstrate that oligomer formation by a mutant htt fragment is strongly polyQ length-dependent, consistent with a causative role for these structures in HD pathogenesis.

2364-Pos**Polymorphism in Alzheimer A β Amyloid Organization: Insight into A β Aggregation**

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Alzheimer disease (AD) is a progressive neurodegenerative disease associated with accumulation of aggregated A β_{1-40} /A β_{1-42} peptides in the brain. Ordered aggregates can extend into β -strand enriched fibrils, regardless of their initial native conformational states. To date, the self-assembly mechanism leading to ordered fibril formation is not fully understood. Understanding the mecha-

nisms and the range of structural features of the aggregates are of crucial importance for effective drug design to reduce aggregate formation. The polymorphism of A β_{1-42} based on ssNMR, EM, 2D hydrogen exchange and mutational studies, was investigated using all-atom molecular dynamics simulations with explicit solvent. Open questions relate to (1) how the monomeric peptides assemble into oligomers; (2) which segments of a long peptide constitute the recognition motifs and as such playing key roles in amyloid fibril formation; (3) how the β -strands arrange relative to one another; (3) is there a favored organization between the β -sheets and if so as one would expect (4) what is it and what are the intermolecular interactions between the layers that stabilize the favored amyloid fibril organization(s) are discussed. This project has been funded in whole or in part with Federal funds from the NCI, NIH, under contract number HHSN261200800001E.

2365-Pos**Structural Determinants of Amyloid B-Protein Oligomerization**

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The oligomerization of amyloid β -protein (A β) is a seminal event in the neurodegenerative process in Alzheimer's disease (AD). A β_{40} and A β_{42} , the two predominant forms of A β , display different aggregation behavior which underlies the special pathogenetic significance of A β_{42} . Previous computational studies have revealed that a turn-like structure exists at the C-terminal of A β_{42} that is not observed in A β_{40} . We report here results of studies to define the structure of this turn and to establish its role in A β assembly. We used molecular dynamics to simulate the structure of the A β C-terminus (Gly31-Val40/Ala42) and discovered that the dihedral angles of residues 36 and 37 tend to be locked into a region of Ramachandran space consistent with type-II β -turns. A β_{31-42} predominantly formed a β -hairpin-like structure that was stabilized by hydrogen bonds and hydrophobic interactions between residues 31-35 and residues 38-42. In contrast, A β_{31-40} appeared relatively unstructured. To investigate the possible role of this peptide-specific, β -hairpin-like structure in A β assembly, we synthesized a number of A β "mutants" containing amino acid substitutions that we postulated would stabilize or destabilize the hairpin. The stabilizing substitutions facilitated hexamer and dodecamer formation by A β_{42} , abolishing formation of fibrils. Interestingly, compared to wild type A β_{42} , these substituted peptides were equally toxic. When these substitutions were incorporated into A β_{40} , the modified A β_{40} oligomerized like A β_{42} , instead of an "A β_{40} -like" distribution. In addition, the modified A β_{40} was significantly more toxic than wild type A β_{40} . Substitutions in A β_{42} that were predicted to destabilize the turn abolished hexamer and dodecamer formation and resulted in an A β_{42} oligomer size distribution similar to that of A β_{40} . Our experiments appear to define the structural determinant that "makes A β_{42} A β_{42} ." If true, this structure would be an exceptionally important therapeutic target.

2366-Pos**A Solid-State NMR Study Reveals Structure and Dynamics in Copper(ii)-Binding to Alzheimer's Beta-Amyloid Fibrils**

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β -amyloid (A β) peptide associated with Alzheimer's diseases exhibit neural toxicity upon aggregation. One of the most widespread hypotheses on the origin of the toxicity of A β aggregates is the binding of Cu²⁺ ions to A β fibrils and subsequent generation of reactive oxygen species (ROS) such as H₂O₂ by Cu²⁺-bound A β . Although a variety of studies have been performed on Cu²⁺-binding to A β , the proposed binding sites or models have been controversial partly because non-crystalline and insoluble nature of A β fibrils have limited access to site-specific structure and dynamic properties on Cu²⁺-bound A β fibrils. Here, we examine the effect of Cu²⁺ binding to amyloid fibrils of 40-residue A β (1-40) by UV-VIS spectroscopy and solid-state NMR (ssNMR). Specifically, we will answer the following questions (i) Is the Cu²⁺ binding is site specific? (ii) If so, which sites are involved in binding? (iii) Are there any major structural changes introduced by Cu²⁺ binding or oxidation due to Cu²⁺?

UV-VIS spectroscopy showed that Cu²⁺ binds to A β (1-40) fibrils almost completely when the ratio of Cu²⁺ to A β (1-40) is less than 1. Based on the result, we performed high-resolution ssNMR experiments on Cu²⁺-bound A β (1-40) fibrils. First, the ¹³C T₁ paramagnetic relaxation enhancement (PRE) due to Cu²⁺ binding on A β was measured for different residues; the PRE data highlight possible binding sites, where the relaxation enhancements are notable. The analysis indicates that the binding is specific, and Cu²⁺ most likely binds to His-13/14 and His-6. Second, the comparison of 2D ¹³C/¹³C correlation spectra of A β fibrils with and without Cu²⁺ revealed that the secondary structure of A β (1-40) fibrils is largely unaltered by Cu²⁺ binding. Third, we tested